

1/11

POSITIONS SEQ ID
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 216-391 31
 194-368 30
 1-178 33

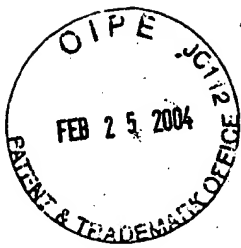
cons.aa	G G G V	A K	E
htGFBR-II	LDTLVGKGRFAEVYKAKLKONTSEQFETVAVKIFPYDHYASWDRKDIFSDINLGHENILQF		
mActR-IIB	LLEIKARGRFGCVWKAQLMN-----DFVAVKIKPLQDKQSWQSEREIFSTPGMCHENILQF		
mActR-II	LLEVKARGRFGCVWKAQLLN-----EYVAVKIFPIQDKQSWQNEYEVYSIPGMCHENILQF		
daf-1	LTVRVGSGRFGNVSRGDYRG-----EAVAVKVFNAIDEPAFHKEIEIFETRMRLRHPNVLRY		
subdomains	I	II	III IV

htGFBR-II	LTAERKTELKQYWLITAFHAKGNLQEYLTRHVISWEDLRNVGSSLARGLSHLSDHTP-C
mActR-IIB	IAAEKRGSNLEVELWLITAFHDKGSLIDYLKQNIITWNELCHEVETMSRGISYLVHEDVPWCR
mActR-II	IGAERKGTSDVDLWLITAFHEKGSLSDFLKANVVSWNELCHIAETMARGLAYLHEDI PGLK
daf-1	IGSDRVDTGFTLWLVI EYHPGSLHDFLENTVNIETYYNLMRSTASGLAFLHNQIGGSK
subdomains	V VI-A

cons.aa	DLK N	DFG
htGFBR-II	GRPKMPIVHRDLKSSNLLVKNDLTCCLCDFGLSLRL---	GPYSSVDDLANSQGVGTARYMAP
mActR-IIB	GECHKPSIAHRDFKSKNVLLKSDLTAVLADFGGLAVRF---	EPGKPPGD--THQGVGTTRYMAP
mActR-II	DGHKPAISHRDIKSKNVLLKQNLTACIADFGGLALKF---	EAGKSACD--THQGVGTTRYMAP
daf-1	ESNKPAMAHARDIKSKNIMYKDLTCAIGDLGLSLSKPEDAASDI IAN--	ENYKCGTVRYLAP
subdomains	VI-B	VII VIII

Fig. 1

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a.a C C E G N M C

5' GCGGATCCTGTTGTGAAGGNAATATGTG 3' Fig. 2A SEQ ID NO: 19

BAMHI C C G C

a.a V A V K I F

5' GCGGATCCGTCGCAGTCAAAATTTT 3' Fig. 2B SEQ ID NO: 20

BamHI G C G G C

T T T A

a.a R D I K S K N

5' GCGGATCCGCGATATTAAAAGCAA 3' Fig. 2C SEQ ID NO: 21

BAMHI A C C GTCT

G A

a.a E P A M Y

5' CGGAATTCTGGTGCCATATA Fig. 2D SEQ ID NO: 22

EcoRI G G G

A A

Seq ID
No

30 31 32 10 24 94 90

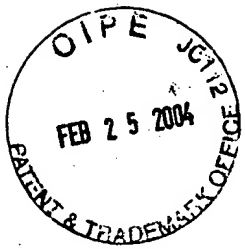
30 31 32 10 24 26 28

30 31 32 10 2 4 6 8 10

[illegible][illegible]

ACR-11
ACR-11B
16R-11
16R-1/ALK-5
ALK-1
ALK-2
ALK-3
ALK-4
ALK-6

Fig. 3 contd.



5810A0

30
31
32
10
2
4
6
8
15

K	M	N	L	T	A	C	I	A	D	F	G	L	A	L	K	F	E	A	G	K	S	A	G	D	-	-	T	H	G	Q	V	G	T	R	R	Y	M	A	P	E	V	L	E	G	ACTR-II
K	S	D	L	T	A	V	L	A	D	F	G	L	A	V	R	F	E	P	T	L	S	P	P	D	-	-	T	H	G	Q	V	G	T	R	R	Y	M	A	P	E	V	L	E	G	ACTR-IIIB
K	H	D	L	T	C	C	L	C	D	F	G	L	A	V	R	H	D	S	A	I	D	T	I	D	L	A	N	S	C	Q	V	G	T	R	R	Y	M	A	P	E	V	L	E	S	TSR-II
K	K	N	G	T	C	C	I	A	D	L	G	L	A	V	R	H	S	Q	S	A	I	D	T	I	D	L	A	N	S	C	Q	V	G	T	R	R	Y	M	A	P	E	V	L	D	TSR-I/ALK-5
K	5	N	L	Q	C	C	I	A	D	L	G	L	A	V	R	H	S	Q	S	A	I	D	T	I	D	L	A	N	S	C	Q	V	G	T	R	R	Y	M	A	P	E	V	L	D	ALK-1
K	K	N	G	S	C	C	I	A	D	L	G	L	A	V	R	H	S	Q	S	A	I	D	T	I	D	L	A	N	S	C	Q	V	G	T	R	R	Y	M	A	P	E	V	L	D	ALK-2
K	K	N	G	S	C	C	I	A	D	L	G	L	A	V	R	H	S	Q	S	A	I	D	T	I	D	L	A	N	S	C	Q	V	G	T	R	R	Y	M	A	P	E	V	L	D	ALK-3
K	K	N	G	S	C	C	I	A	D	L	G	L	A	V	R	H	S	Q	S	A	I	D	T	I	D	L	A	N	S	C	Q	V	G	T	R	R	Y	M	A	P	E	V	L	D	ALK-4
K	K	N	G	S	C	C	I	A	D	L	G	L	A	V	R	H	S	Q	S	A	I	D	T	I	D	L	A	N	S	C	Q	V	G	T	R	R	Y	M	A	P	E	V	L	D	ALK-6

VIII

VII

A	I	N	F	Q	R	-	D	A	F	L	R	I	D	M	Y	A	M	G	L	V	L	M	E	L	A	S	R	C	T	A	A	D	G	P	V	D	E	Y	M	L	P	F	E	E	ACTR-II	
A	I	N	F	Q	R	-	D	A	F	L	R	I	D	M	Y	A	M	G	L	V	L	M	E	L	A	S	R	C	T	A	A	D	G	P	V	D	E	Y	M	L	P	F	E	E	ACTR-IIIB	
A	R	M	N	L	E	N	A	E	S	F	K	Q	I	D	V	Y	S	M	A	L	V	L	M	E	L	A	S	R	C	T	A	A	D	G	P	V	D	E	Y	M	L	P	F	E	S	TSR-II
S	I	N	M	K	H	F	E	S	F	K	R	A	D	I	Y	A	M	G	L	V	L	M	E	L	A	S	R	C	T	A	A	D	G	P	V	D	E	Y	M	L	P	F	E	S	TSR-I/ALK-5	
Q	I	R	T	D	C	F	E	S	Y	K	R	T	D	I	M	A	F	G	L	V	L	M	E	L	A	S	R	C	T	A	A	D	G	P	V	D	E	Y	M	L	P	F	E	S	ALK-1	
T	I	Q	V	D	C	F	D	S	Y	K	R	V	D	I	M	A	F	G	L	V	L	M	E	L	A	S	R	C	T	A	A	D	G	P	V	D	E	Y	M	L	P	F	E	S	ALK-2	
S	L	N	K	N	H	F	Q	P	Y	I	M	A	D	I	Y	S	E	G	L	I	I	M	E	L	A	S	R	C	T	A	A	D	G	P	V	D	E	Y	M	L	P	F	E	S	ALK-3	
T	I	N	M	K	H	F	D	S	F	K	R	C	A	D	I	Y	A	L	G	L	V	Y	M	E	L	A	S	R	C	T	A	A	D	G	P	V	D	E	Y	M	L	P	F	E	S	ALK-4
S	L	N	R	M	H	F	Q	S	Y	I	M	A	D	M	Y	S	E	G	L	I	I	M	E	L	A	S	R	C	T	A	A	D	G	P	V	D	E	Y	M	L	P	F	E	S	ALK-6	

X

IX

E	I	G	Q	H	P	S	L	E	D	H	Q	E	V	V	V	H	K	K	K	K	R	R	P	V	L	R	D	Y	W	Q	K	H	A	G	M	A	M	L	C	E	T	I	E	C	W	ACTR-II				
E	I	G	Q	H	P	S	L	E	E	L	Q	E	V	V	V	H	K	K	K	K	R	R	P	V	L	R	D	Y	W	Q	K	H	A	G	M	A	M	L	C	E	T	I	E	C	W	ACTR-IIIB				
K	V	R	E	N	P	C	V	E	S	M	K	D	N	V	L	R	D	R	G	R	P	P	P	E	I	K	S	F	W	L	M	H	Q	I	Q	M	V	C	E	I	L	T	E	C	W	TSR-II				
L	V	P	S	D	P	S	V	E	E	M	R	K	V	V	C	E	Q	K	L	R	P	P	P	I	P	H	R	R	L	A	A	D	P	V	L	S	G	L	A	Q	M	A	K	I	M	R	E	C	W	TSR-I/ALK-5
V	V	P	H	D	P	S	V	E	D	M	R	K	V	V	C	V	D	Q	Q	R	P	P	P	I	P	H	R	R	L	A	A	D	P	V	L	S	G	L	A	Q	M	A	K	I	M	R	E	C	W	ALK-1
V	V	P	H	D	P	S	V	E	D	M	R	K	V	V	C	V	D	Q	Q	R	P	P	P	I	P	H	R	R	L	A	A	D	P	V	L	S	G	L	A	Q	M	A	K	I	M	R	E	C	W	ALK-2
M	V	P	S	D	P	S	V	E	D	M	R	K	V	V	C	V	D	Q	Q	R	P	P	P	I	P	H	R	R	L	A	A	D	P	V	L	S	G	L	A	Q	M	A	K	I	M	R	E	C	W	ALK-3
L	V	P	S	D	P	S	V	E	D	M	R	K	V	V	C	V	D	Q	Q	R	P	P	P	I	P	H	R	R	L	A	A	D	P	V	L	S	G	L	A	Q	M	A	K	I	M	R	E	C	W	ALK-4
L	V	P	S	D	P	S	V	E	D	M	R	K	V	V	C	V	D	Q	Q	R	P	P	P	I	P	H	R	R	L	A	A	D	P	V	L	S	G	L	A	Q	M	A	K	I	M	R	E	C	W	ALK-6

Fig. 3 contd.



SEALING

30
31
32
10 2 + 3600

ACTR-11
ACTR-11B
YGR-11
YGR-1/ALK-5
ALK-1
ALK-2
ALK-3
ALK-4
ALK-6

Y I N V D F P
I I N V D L L
C S L T T

V T V V
V S L V
E E K I

(503)
(509)

I I T E D I
C T Y S D C L
L S G R S C S
I K M (503)
X P K V I Q
X X L K Y D C
V V K I (532)
V V K I (505)
K I (502)

N N R G E D D D D
 Y V R G E P L Q E Q
 L S L Q S S S Q
 R R H Q N S N E V F
 Q R E S S D V S S
 M I L L I I M L M

	S	S	Q	T	A	S	A
I	V	L	L	L	L	L	L
R	E	R	T	L	L	L	L
E	E	R	T	L	L	L	L
G	E	E	K	K	K	K	K
V	V	A	K	K	K	K	K
			I	I	I	I	I
							V

A G G G
 A G G G
 S S T T T T T T
 L L L L L L L L
 R R R R R R R R
 A A A A A A S A

E A E A
 A A P G S S A A
 O O O N N N P A
 H H H A P Q H A
 O O O Y Y Y A Y

P K E S S L (S13)
P K E S S I (S36)
K (S67)

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Fig. 3 contd.

[illegible]

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Fig. 5.